

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCGGCGCT	CGGCGCTGCG	GGTGGCTGCG	CTGCTGCTAC	CGCTGCTGTG	GCTACTGCTG	60
MetProProS	erGlyLeuAr	gLeuLeuPro	LeuLeuLeuP	roLeuLeuTr	pLeuLeuVal	
CTGACGCGCTG	GGCGCGCGCG	CGGCGGACTA	TCCACCTGCA	AGACTATGCA	CATGGAGCTG	120
LeuThrProG	lyProProAl	aAlaGlyLeu	SerThrCysL	ysThrIleAs	pMetGluLeu	
GTGAAGCGGA	AGCGCATGCA	GGCCATCGGC	GGCCAGATCC	TGTCCAAGCT	GCGGCTCGCC	180
ValLysArgL	ysArgIleGl	uAlaIleArg	GlyGlnIleL	euSerLysLe	uArgLeuAla	
AGCGCGCGCA	GCCAGCGCGA	GGTGGCGCGC	GGCGCGCTGC	CGGAGCGCGT	GCTCGCGCGT	240
SerProProS	erGlnGlyGl	uValProPro	GlyProLeuP	roGluAlaVa	lLeuAlaLeu	
TACAACAGCA	CCCGCGACCG	GGTGGCGCGG	GAGAGTGCAG	AACCGGAGCC	CGAGCGTGAG	300
TyrAsnSerT	hrArgAspAr	gValAlaGly	GluSerAlaG	luProGluPr	oGluProGlu	
GGCGACTACT	ACGCCAAGGA	GGTCAACCGC	GTGCTAATGG	TGGAAACCCA	CAACGAAATC	360
AlaAspTyrT	yrAlaLysGl	uValThrArg	ValLeuMetV	alGluThrHi	sAsnGluIle	
TATGACAAGT	TCAAGCAGAG	TACACACAGC	ATATATATGT	TCTTCAACAC	ATCAGAGCTC	420
TyrAspLysP	heLysGlnSe	rThrHisSer	IleTyrMetP	hePheAsnTh	rSerGluLeu	
CGAGAAGCGG	TACCTGAACC	CGTGTTCCTC	TCCCGGCGAG	AGCTGGCTCT	GCTGAGGAGG	480
ArgGluAlaV	alProGluPr	oValLeuLeu	SerArgAlaG	luLeuArgLe	uLeuArgArg	
CTCAAGTTAA	AAGTGGAGCA	GCACGTGGAG	CTGTACCAGA	AATACAGCAA	CAATTCCTGG	540
LeuLysLeuL	ysValGluGl	nHisValGlu	LeuTyrGlnL	ysTyrSerAs	nAsnSerTrp	
CGATACTCA	GCAACCGCGT	GCTGGCAACC	AGCGACTCGC	CAGAGTGGTT	ATCTTTTGAT	600
ArgTyrLeuS	erAsnArgLe	uLeuAlaPro	SerAspSerP	roGluTrpLe	uSerPheAsp	
GTACCGCGAG	TTGTGGCGCA	GTGGTGGAGC	CGTGGAGGGG	AAATGGAGGG	CTTTGCGCTT	660
ValThrGlyV	alValArgGl	nTrpLeuSer	ArgGlyGlyG	luIleGluGl	yPheArgLeu	
AGCGCGCACT	GCTCTGTGTA	CAGCAGGGAT	AACACACTGC	AAGTGGACAT	CAACGGGTTC	720
SerAlaHisC	ysSerCysAs	pSerArgAsp	AsnThrLeuG	lnValAspIl	eAsnGlyPhe	
ACTACCGGOC	GGCGAGGTGA	CCTGGCCACC	ATTATGGGCA	TGAACCGGOC	TTTCTGCTT	780
ThrThrGlyA	rgArgGlyAs	pLeuAlaThr	IleHisGlyM	etAsnArgPr	oPheLeuLeu	
CTCATGGCCA	CCCGCTGGA	GAGGGGCGAG	CATCTGCAAA	GCGAATTGGG	GCGAGGCGGA	840
LeuMetAlaT	hrProLeuGl	uArgAlaGln	HisLeuGlnS	erGluPheGl	yGlyGlyGly	
TCCCGGCTCG	GGCTTTGGGC	GGGAGGGGGC	TCCCGGCGCG	CAATCAACTA	TAAAGAGCTC	900
SerProLeuG	lyLeuTrpAl	aGlyGlyGly	SerAlaAlaA	laIleAsnTy	riysGlnLeu	
CAGCTCCAAG	AAAGGACGAA	CATTGGGAAA	TGTACGGAGC	TCTTGGAGCA	GCTGAATGGA	960
GlnLeuGlnG	luArgThrAs	nIleArgLys	CysGlnGluL	euLeuGluGl	nLeuAsnGly	

Fig. 1

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
AAGATCAACC	TCACTACAG	GGCGGACTTC	AAGATCCCTA	TGGAGATGAC	GGAGAAGATG	1020
LysIleAsnL	euThrTyrAr	gAlaAspPhe	LysIleProM	etGluMetTh	rGluLysMet	
CAGAAGAGTT	ACACTGCTTT	TGCCATCCAA	GAGATGCTCC	AGAATGTCTT	TCTTGTCCTC	1080
GlnLysSerT	yrThrAlaPh	eAlaIleGln	GluMetLeuG	lnAsnValPh	eLeuValPhe	
AGAAACAATT	TCTCCAGCAC	TGGGTGGAAT	GAGACTATTG	TTGTACGICT	CCTGGATGAA	1140
ArgAsnAsnP	heSerSerTh	rGlyTrpAsn	GluThrIleV	alValArgLe	uLeuAspGlu	
CTCCACCAGC	AGACAGTGT	TCIGAAGACA	GTACTAGAGG	AAAAGCAAGA	GGAAAGATTG	1200
LeuHisGlnG	lnThrValPh	eLeuLysThr	ValLeuGluG	luLysGlnGl	uGluArgLeu	
AAGTGGGAGA	TGTCTCAAC	TGCTCTCCAC	TTGAAGAGCT	ATTACTGGAG	GGTGCAAAGG	1260
ThrTrpGluM	etSerSerTh	rAlaLeuHis	LeuLysSerT	yrTyrTrpAr	gValGlnArg	
TACCTTAAAC	TCATGAAGTA	CAACAGCTAC	GCCTCGATCG	TGGTCCGAGC	AGAGATCTTC	1320
TyrLeuLysL	euMetLysTy	rAsnSerTyr	AlaTrpMetV	alValArgAl	aGluIlePhe	
AGGAACCTTC	TCATCATTCG	AAGACTTACC	AGAAACTTCC	AAAACGTATC	TAGACC	1376
ArgAsnPheL	euIleIleAr	gArgLeuThr	ArgAsnPheG	lnAsn...Se	rArg	
				uga		

0055201001

Fig. 2

lfn+MMP+TGFb Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GTGTTGCTCT	CCCGGSCAGA	GCTGGGCTCTG	CTGAGGAGGC	TCAAGTTAAA	AGTGGAGCAG	1020
ValLeuLeuS	erArgAlaGl	uLeuArgLeu	LeuArgArgL	euLysLeuLy	sValGluGln	
CACGTGGAGC	TGTAACAGAA	ATACAGCAAC	AATTOCTGGC	GATAOCTCAG	CAACCGGCTG	1080
HisValGluL	euTyrGlnLy	sTyrSerAsn	AsnSerTrpA	rgTyrLeuSe	rAsnArgLeu	
CTGGCAOCCA	GCGACTGGCC	AGAGTGGTTA	TCTTTTGATG	TCACCGGAGT	TGTGGCGCAG	1140
LeuAlaProS	erAspSerPr	oGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	
TGGTTGAGCC	GTGGAGGGGA	AATTGAGGGC	TTTGGCCTTA	GCGCCCACTG	CTCCTGTGAC	1200
TrpLeuSerA	rgGlyGlyGl	uIleGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
AGCAGGGATA	ACACACTGCA	AGTGGACATC	AACGGGTICA	CTACCGGCGG	CCGAGGTGAC	1260
SerArgAspA	snThrLeuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
CTGGCCACCA	TTCATGGCAT	GAACCGGCTT	TTCTGTCTTC	TCATGGCCAC	CCCGCTGGAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	PheLeuLeuL	euMetAlaTh	rProLeuGlu	
AGGGCCACAG	ATCTGCAAAG	CtgaTCTAGA	CC			1352
ArgAlaGlnH	isLeuGlnSe	r...SerArg				

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      1          20          40          60
Hu TGF-β 1  MPPSGRLRLPLLLPLLLV-LTPGPPAAGLSTCKTIDMELVKKR|EATRGQILSKRLASPPSOGE-VP-PGP
Hu TGF-β 2  MHYCVLSAFLILH  LVTVAL-----SLSTCSYLMDQFMKKR|EATRGQILSKRLTSPP---EDYPEPEE
Hu TGF-β 3  MKHMLQRLVVLALLNFATVSL-----SLSTCTTLDYGHKKKKVE|EATRGQILSKRLTSPP---EPTV-MTH
Ck TGF-β 4  -----
Fg TGF-β 5  MEV-----LHMLLVLLV-LHLSLAMSISTCKAVDHEEVKKR|EATRGQILSKRLDKTPOVDS-EK-NTV
      +      +      +      +      +      +      +      +      +      +      +
      80          100         120
Hu TGF-β 1  LPEAVLALYHSTIRDVACESAEPE-PEP-----EADYYAKEVTRVLNV---ETHHEIYDKFKQSTHSIYHFF
Hu TGF-β 2  YPPEVISIYHSTIRDL--QEKASR-RAACERERSDEEYAKEVYKIDMPFFPS-ENAIPTFYQPY-FRIVRF
Hu TGF-β 3  YPYQVLALYHSTIRELL--FENGER-KEEGCTQENTSEYAKE|HAFDMIGGLAE-HNELAVCPKGI-SKVYRF
Ck TGF-β 4  -----M--DPKSTGPK--SCG-----GSPW-RPP-GTAPWSIG-SR--RA
Fg TGF-β 5  PSEALF-LYHSTILE-VIREKATRE-EEHVGHQDQIQQYAKQVYRF---ESITELEDHETKFK-----F
      +      +      +      +      +      +      +      +      +      +
      140         160         180
Hu TGF-β 1  MISEL-----RE-AVPEPVLLS-RAELHLLRLKL---KV-EQHYELYQ-----KYSKNSWRYLSHRLAPSDSPE
Hu TGF-β 2  DVSA-----MEKHASHLV-KAEFRVRLQHPK-AAPVEQRIELYQILSKDLTPTQRYIDSKVVKTRAECE
Hu TGF-β 3  NYSS-----VEKHRLNLF-RAEFVRLVPPNP-SKRNEQRIELFQILRP-DEHIAQRTYIGGKMLPTGTAE
Ck TGF-β 4  TASSCSSTSSRAEYGGRAILLHRAELRLRQKAAASAGTEQRLLEYQGYG-----NASHWRYLNGRSVRATADE
Fg TGF-β 5  HASKV----RENVGMW-SLLH-NAELRMKY-KQID--KVMQRMELFW--KYQENGTHSRYLESKYITPVTDGE
      +      +      +      +      +      +      +      +      +      +
      200         220         240
Hu TGF-β 1  WLSFDYTGYYVOWLSRGGEIEGFRLSAHCSG-----DSRQMTLQVDIN-GFTTGR-----RQDLATT-----
Hu TGF-β 2  WLSFDYTDVAVHEWLHKKDRNLGFKISLHCPGCTFVPSHNYTIPNKSEELARFA-GIDGISTYSSQDKYIKSTRK
Hu TGF-β 3  WLSFDYTDVREWLRRRESNLGLEISIMCPCHTFOP-NGDILENHEYMETKFK-GVDHEDONGRGLGRLK---K
Ck TGF-β 4  WLSFDYTDVAVHOMLSGSELLGVFKLSYHCPCHGPG-HADENRISIEGFEQQ-----RQDMOSTA---K
Fg TGF-β 5  WLSFDYTKTVNEVLKRAEENEQGLQPAKCG-----PTPAKD----IDIEGFAL-RQDLASL--SSK
      +      +      +      +      +      +      +      +      +      +
      260         280         300
Hu TGF-β 1  ---NQMWRPFLLMATPLERA-QH-LOSS---RHRALDINYCFST--EKNCCVPOLYIDFRKDLGWKVINEP
Hu TGF-β 2  KWSGEY---PHLLMLPSTRL-ESQ---QIRKKRALDAAYCFRNV--QDNCLRLPYIDFRKDLGWKVINEP
Hu TGF-β 3  QKQNY--H-PKLLMIPPHRL-DNPGGGQ---RKKRALDINYCFRNL--EENCCVPRLYIDFRKDLGWKVINEP
Ck TGF-β 4  -KRRQ--V-PYVLAMALPAERANE--LHSA---RRRDLOTQYCFGPGTDEKNCVRLPYIDFRKDLGWKVINEP
Fg TGF-β 5  ENT-----KPYL--MITSMPAERIDIVT SS---REKRGVGOETCFGNW--QPHCCVPLTYINFRKDLGWKVINEP
      +      +      +      +      +      +      +      +      +      +
      320         340         360         380         390
Hu TGF-β 1  KGYHANFCLGCPYIWSIDTOYSKVLALYNQUNPGASAPCCVPQALEPLIYVYVGRKPKVEQLSNHIVRSCKCS
Hu TGF-β 2  KGYHANFCAGACPYLWSSDTONSRVLSLYNTINPEASAPCCVSOOLEPLIYVYIGKIPKIEQLSNHIVKSCCKS
Hu TGF-β 3  KGYHANFCGCPYLRADTINSTVLGLYNTLNPEASAPCCVPQOLEPLIYVYVGRTPKVEQLSNHIVVYKSCCKS
Ck TGF-β 4  KGYHANFCNGCPYIWSADTOYEVLAETHOHNPASAPCCVPQOTLDPLIYVYVGRVYRVEQLSNHIVRACKCS
Fg TGF-β 5  KGYEANYCLGCPYIWSMDTOYSKVLALYNQUNPGASISPCCVPOVLEPLIYVYVGRIAKVEQLSNHIVRSCHCS
      +      +      +      +      +      +      +      +      +      +

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Fig. 3

Protein	Sequence	Reference
MMP-1/MMP-8		
Human type I collagen ($\alpha 1$)	Ala-Pro-Gln-Gly ₇₇₅ ~ Ile ₇₇₆ -Ala-Gly-Gln	80
Human type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~ Leu ₇₇₆ -Leu-Gly-Ala	80
Human type II collagen	Gly-Pro-Gln-Gly ₇₇₅ ~ Leu ₇₇₆ -Ala-Gly-Gln	80
Human type III collagen	Gly-Pro-Leu-Gly ₇₇₅ ~ Ile ₇₇₆ -Ala-Gly-Ile	80
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₈₇ ~ Leu ₆₈₈ -Arg-Val-Gly	84
Rat α_2 -macroglobulin	Ala-Ala-Tyr-His ₆₈₁ ~ Leu ₆₈₂ -Val-Ser-Gln	84
Rat α_2 -macroglobulin	Met-Asp-Ala-Phe ₆₈₁ ~ Leu ₆₈₂ -Gln-Ser-Ser	84
Rat α_1 -macroglobulin	Glu-Pro-Gln-Ala ₆₈₃ ~ Leu ₆₈₄ -Ala-Met-Ser	84
Rat α_1 -macroglobulin	Gln-Ala-Leu-Ala ₆₈₅ ~ Met ₆₈₆ -Ser-Ala-Ile	84
Chicken ovostatin	Pro-Ser-Tyr-Phe ₆₇₂ ~ Leu ₆₇₄ -Asn-Ala-Gly	79
Human pregnancy zone protein	Tyr-Glu-Ala-Gly ₆₈₅ ~ Leu ₆₈₆ -Gly-Val-Val	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₆₈₇ ~ Val ₆₈₈ -Val-Glu-Arg	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₇₅₇ ~ Ile ₇₅₈ -Ser-Ser-Thr	84
α_1 -Protease inhibitor	Gly-Ala-Met-Phe ₃₅₂ ~ Leu ₃₅₃ -Glu-Ala-Ile	85
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	86
Human aggrecan	Thr-Glu-Gly-Glu ₃₇₃ ~ Ala ₃₇₄ -Arg-Gly-Ser	86
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~ Ile ₁₇ -Gln-Ala-Glu	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₀ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-2		
Guinea pig $\alpha 1(I)$ gelatin	Gly-Ala-Hyp-Gly ₃₄₇ ~ Leu ₃₄₈ -Glx-Gly-His	24
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Gln-Gly ₁₀₀ ~ Val ₁₀₁ -Arg-Gly-Glu	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ala-Gly ₂₇₇ ~ Val ₂₇₈ -Gln-Gly-Pro	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ser-Gly ₃₆₁ ~ Leu ₃₆₂ -Hyp-Gly-Pro	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ala-Gly ₃₇₇ ~ Glu ₃₇₈ -Arg-Gly-Ser	30
Rat $\alpha 1(I)$ gelatin	Gly-Ala-Lys-Gly ₃₈₁ ~ Leu ₃₈₂ -Thr-Gly-Ser	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ala-Gly ₃₈₂ ~ Gln ₃₈₃ -Asp-Gly-Pro	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ala-Gly ₃₈₄ ~ Phe ₃₈₅ -Ala-Gly-Pro	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Ile-Gly ₅₇₆ ~ Asn ₅₇₇ -Val-Gly-Ala	30
Rat $\alpha 1(I)$ gelatin	Gly-Pro-Hyl-Gly ₆₁₂ ~ Ser ₆₁₃ -Arg-Gly-Ala	30
Bovine type I collagen ($\alpha 1$)	Gly-Pro-Gln-Gly ₇₇₅ ~ Ile ₇₇₆ -Ala-Gly-Gln	22
Bovine type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~ Leu ₇₇₆ -Leu-Gly-Ala	22
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₄₂ ~ Tyr ₆₁ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~ Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₃ ~ Leu ₂₄ -Val-Glu-Ala	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₀ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-3		
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₈₇ ~ Leu ₆₈₈ -Arg-Val-Gly	79
Human α_2 -macroglobulin	Arg-Val-Gly-Phe ₆₈₄ ~ Tyr ₆₈₅ -Glu-Ser-Asp	79
Human α_1 -antichymotrypsin	Leu-Leu-Ser-Ala ₃₆₀ ~ Leu ₃₆₁ -Val-Glu-Thr	91
α_1 -protease inhibitor	Glu-Ala-Ile-Pro ₃₃₇ ~ Met ₃₃₈ -Ser-Ile-Pro	91
Antithrombin III	Ile-Ala-Gly-Arg ₃₂₅ ~ Ser ₃₂₆ -Leu-Asn-Pro	91
Chicken ovostatin	Leu-Asn-Ala-Gly ₆₇₇ ~ Phe ₆₇₈ -Thr-Ala-Ser	79, 92
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~ Phe ₃₄₂ -Phe-Gly-Val	93
Substance P	Lys-Pro-Gln-Gln ₄ ~ Phe ₇ -Phe-Gly-Leu	37
Human ProMMP-1	Asp-Val-Ala-Gln ₃₈ ~ Phe ₆₁ -Val-Leu-Thr	43
Human ProMMP-3	Asp-Thr-Leu-Glu ₆₁ ~ Val ₆₂ -Met-Arg-Lys	94
Human ProMMP-3	Asp-Val-Gly-His ₆₂ ~ Phe ₆₃ -Arg-Thr-Phe	94
Human ProMMP-8	Asp-Ser-Gly-Gly ₇₁ ~ Phe ₇₂ -Met-Leu-Thr	95
Human ProMMP-9	Arg-Val-Ala-Glu ₄₀ ~ Met ₄₁ -Arg-Gly-Glu	48
Human ProMMP-9	Asp-Leu-Gly-Arg ₆₇ ~ Phe ₇₀ -Gln-Thr-Phe	48
Human fibronectin	Pro-Phe-Ser-Pro ₆₄ ~ Leu ₆₆₀ -Val-Ala-Thr	21

Fig. 4

	Sequence	Reference
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₀ ~Leu ₁₀₀ -Leu-Pro-Ala Ala-Pro-Gly-Asn ₁₀₀ ~Ala ₁₁₀ -Ser-Glu-Ser Phe-Ser-Ser-Glu ₁₁₀ ~Ser ₁₁₇ -Lys-Arg-Glu	88 88 88
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Ala-Gly-Gly-Ala ₁₁₃ ~Gln ₁₁₆ -Met-Gly-Val	96
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Gln-Met-Gly-Val ₁₁₉ ~Met ₁₂₀ -Gln-Gly-Pro	96
Bovine $\alpha 1$ (IX) collagen, NC2	Met-Ala-Ala-Ser~Leu-Lys-Arg-Pro	96
Bovine $\alpha 2$ (IX) collagen, NC2	~Ala-Lys-Arg-Glu	96
Bovine $\alpha 3$ (IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine $\alpha 1$ (XI) collagen, N- telopeptide	Gln-Ala-Gln-Ala~Ile-Leu-Gln-Gln	96
Human cartilage link	Arg-Ala-Ile-His ₁₀ ~Ile ₁₇ -Gln-Ala-Glu	87
Bovine insulin, B chain	Leu-Val-Glu-Ala ₁₄ ~Leu ₁₅ -Tyr-Leu-Val	97
Bovine insulin, B chain	Glu-Ala-Leu-Tyr ₁₆ ~Leu ₁₇ -Val-Cys-Gly	21, 97
MMP-7		
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human cartilage link	Gly-Pro-His-Leu ₃₃ ~Leu ₃₆ -Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glu ₁₄₃ ~Leu ₁₄₄ -Lys-Phe-Gln	98
MMP-9		
Human type V collagen ($\alpha 1$)	Gly-Pro-Pro-Gly ₄₃₇ ~Val ₄₄₀ -Val-Gly-Pro	99
Human type V collagen ($\alpha 2$)	Gly-Pro-Pro-Gly ₄₄₅ ~Leu ₄₄₆ -Arg-Gly-Glu	99
Human type XI collagen ($\alpha 1$)	Gly-Pro-Gly-Gly ₄₃₇ ~Val ₄₄₀ -Val-Gly-Pro	99
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₀ ~Ile ₁₇ -Gln-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ala-Ile-His ₁₀ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₃ ~Leu ₂₆ -Val-Glu-Ala	87

A.



B.

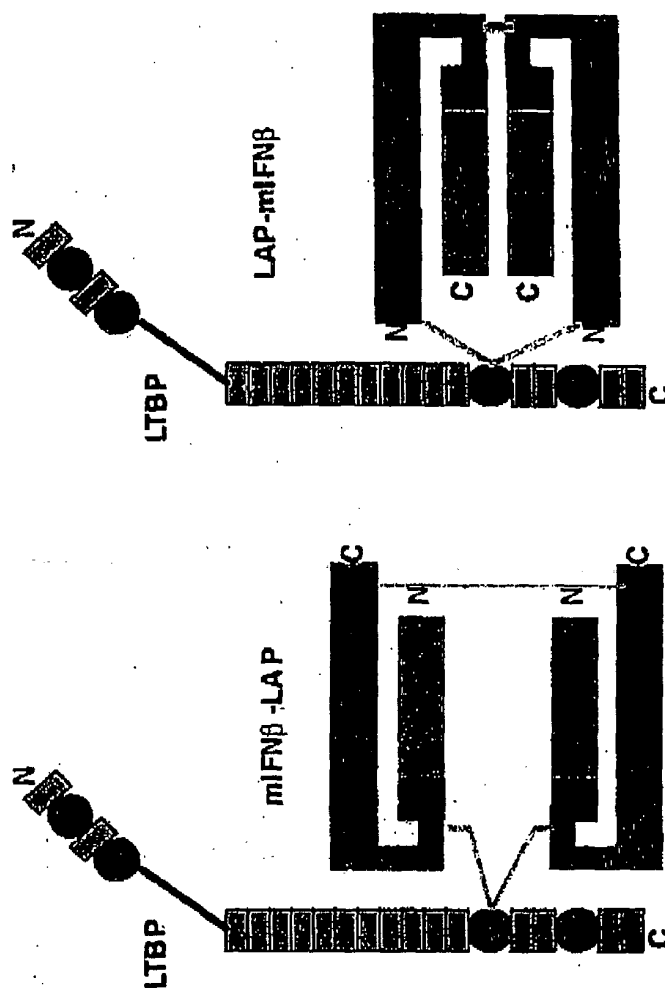


Fig. 5

TO60T0-E829260

M.W. 1 2 3

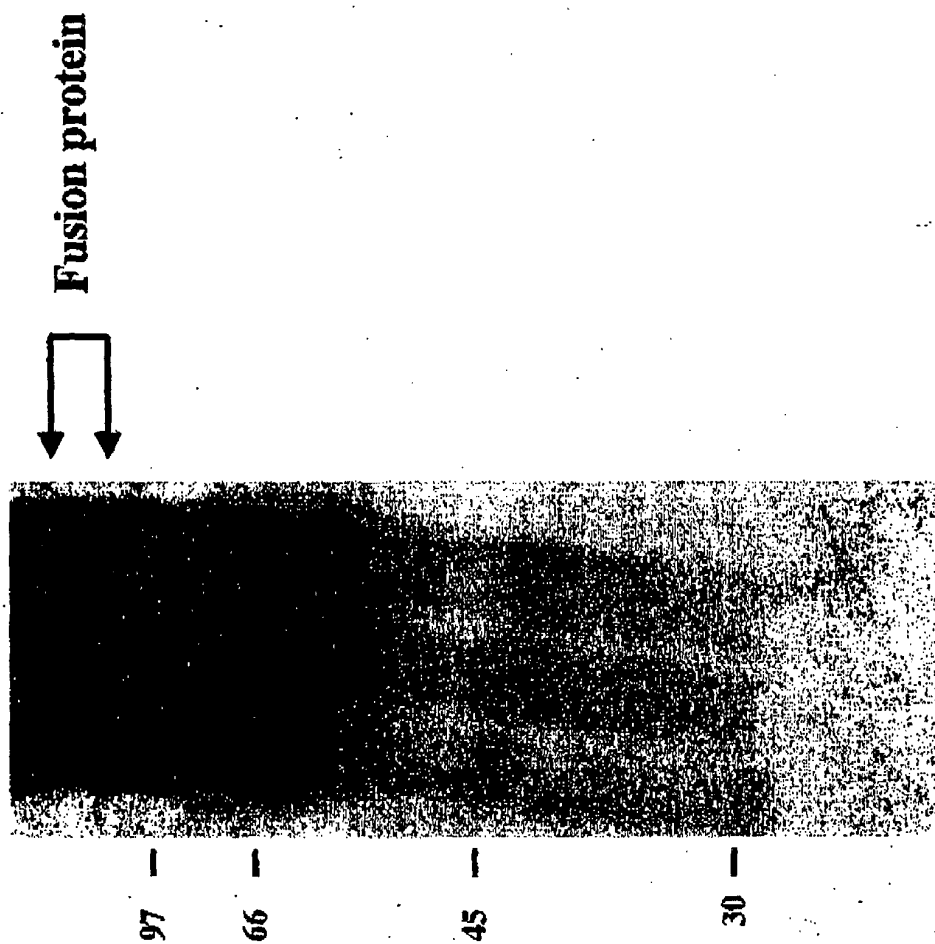


Fig. 6

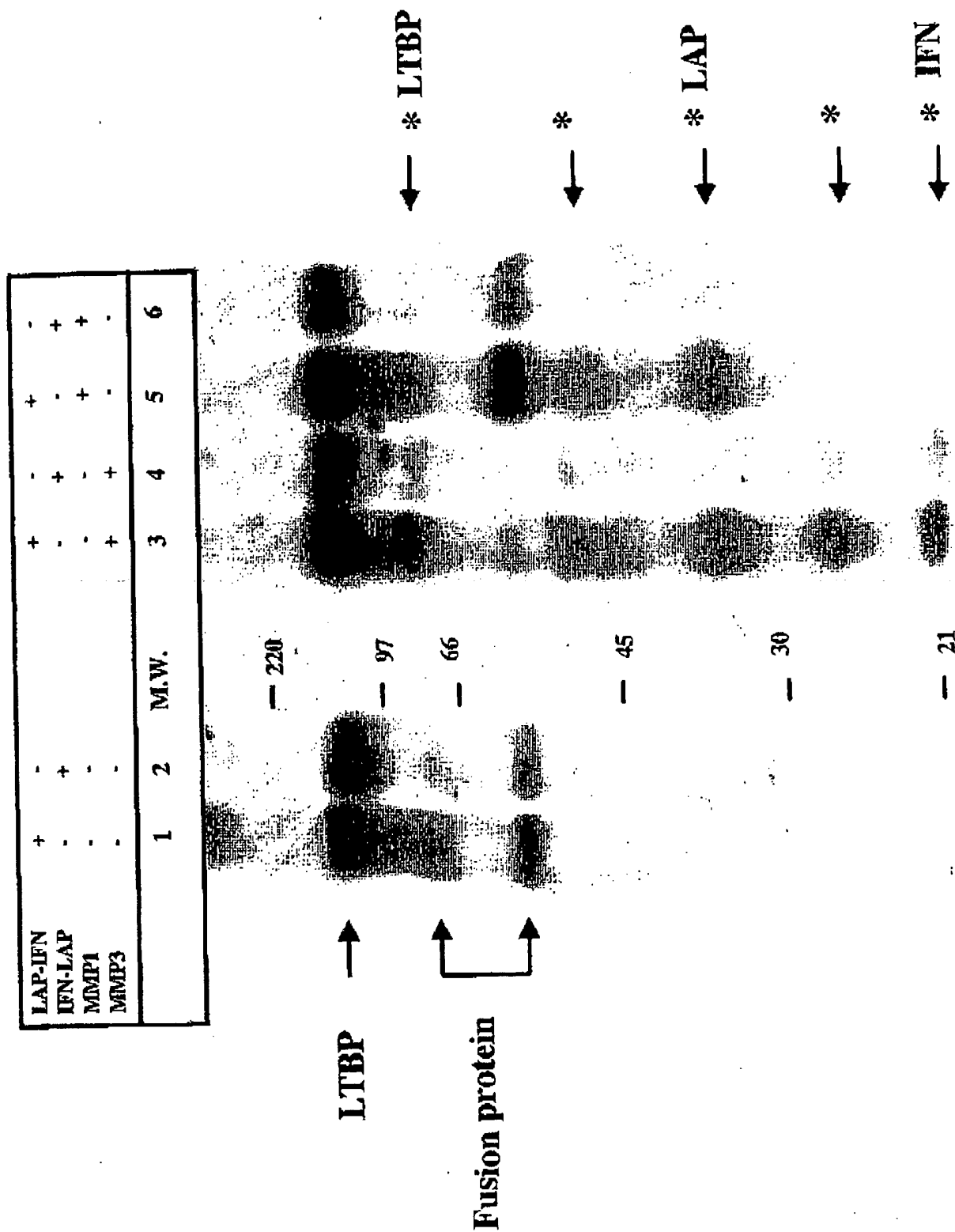


Fig. 7

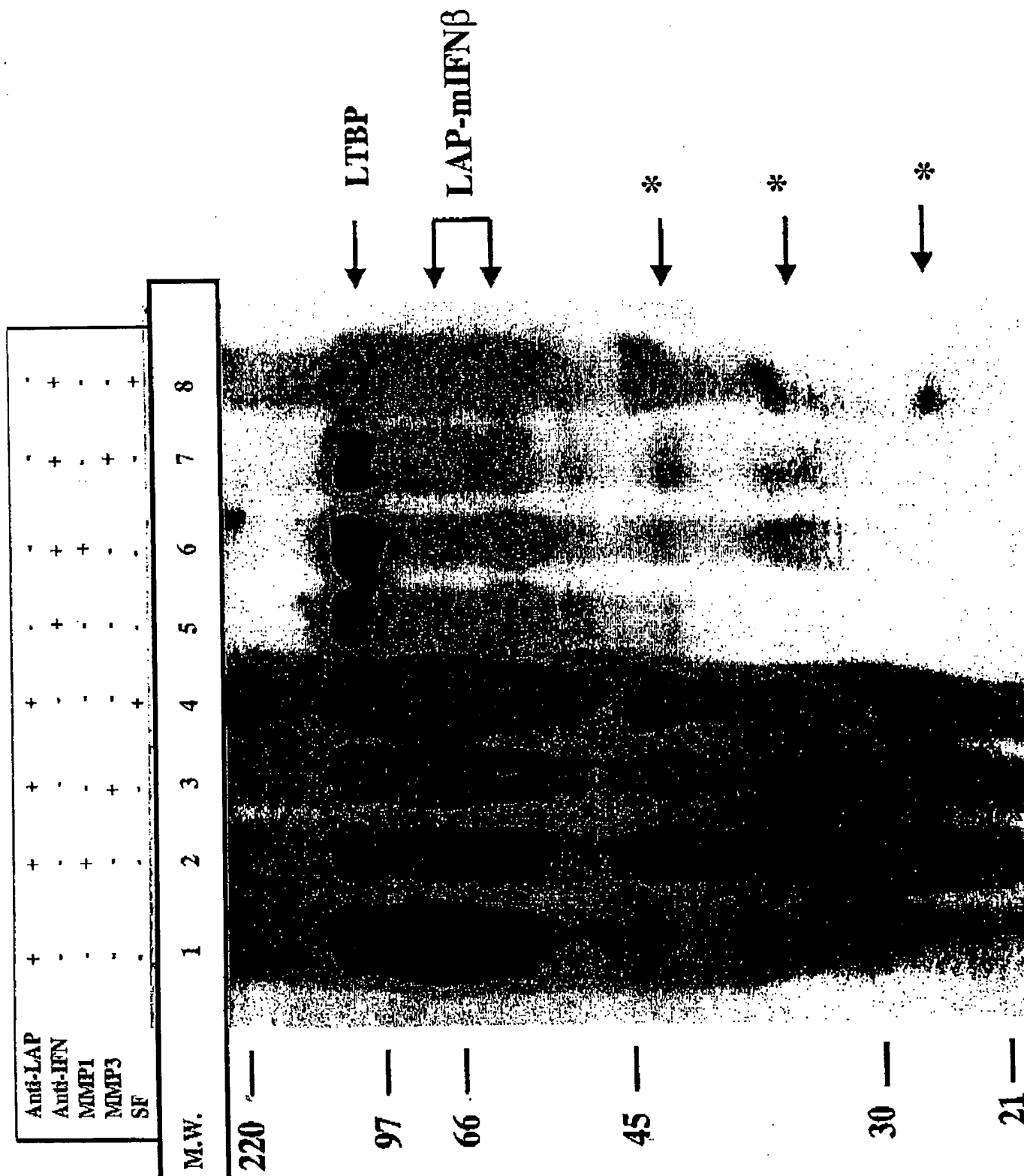


Fig. 8a

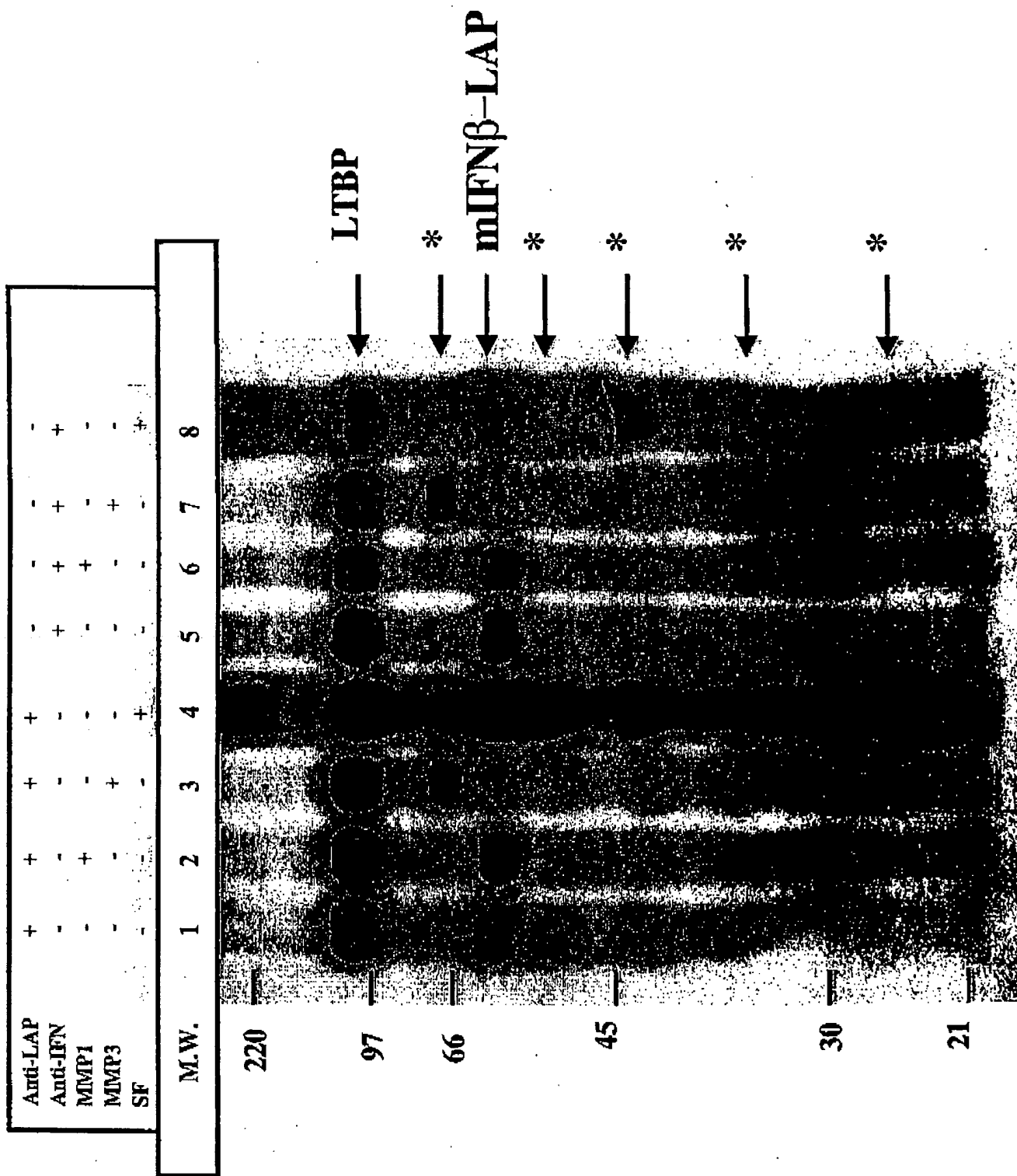


Fig. 8b

